```
ATGGCTTTGG AACAGAACCA GTCAACAGAT TATTATTATG AGGAAAATGA          50
M  A  L  E   Q  N  Q   S  T  D   Y  Y  Y  E   E  N  E

AATGAATGGC ACTTATGACT ACAGTCAATA TGAACTGATC TGTATCAAAG         100
 M  N  G   T  Y  D  Y   S  Q  Y   E  L  I   C  I  K  E

AAGATGTCAG AGAATTTGCA AAAGTTTTCC TCCCTGTATT CCTCACAATA         150
  D  V  R   E  F  A   K  V  F  L   P  V  F   L  T  I

GTTTTCGTCA TTGGACTTGC AGGCAATTCC ATGGTAGTGG CAATTTATGC         200
V  F  V  I   G  L  A   G  N  S   M  V  V  A   I  Y  A

CTATTACAAG AAACAGAGAA CCAAAACAGA TGTGTACATC CTGAATTTGG         250
 Y  Y  K   K  Q  R  T   K  T  D   V  Y  I   L  N  L  A

CTGTAGCAGA TTTACTCCTT CTATTCACTC TGCCTTTTTG GGCTGTTAAT         300
  V  A  D   L  L  L   L  F  T  L   P  F  W   A  V  N

GCAGTTCATG GGTGGGTTTT AGGGAAAATA ATGTGCAAAA TAACTTCAGC         350
A  V  H  G   W  V  L   G  K  I   M  C  K  I   T  S  A

CTTGTACACA CTAAACTTTG TCTCTGGAAT GCAGTTTCTG GCTTGTATCA         400
 L  Y  T   L  N  F  V   S  G  M   Q  F  L   A  C  I  S

GCATAGACAG ATATGTGGCA GTAACTAAAG TCCCCAGCCA ATCAGGAGTG         450
  I  D  R   Y  V  A   V  T  K  V   P  S  Q   S  G  V

GGAAAACCAT GCTGGATCAT CTGTTTCTGT GTCTGGATGG CTGCCATCTT         500
G  K  P  C   W  I  I   C  F  C   V  W  M  A   A  I  L

GCTGAGCATA CCCCAGCTGG TTTTTTATAC AGTAAATGAC AATGCTAGGT         550
 L  S  I   P  Q  L  V   F  Y  T   V  N  D   N  A  R  C

GCATTCCCAT TTTCCCCCGC TACCTAGGAA CATCAATGAA AGCATTGATT         600
  I  P  I   F  P  R   Y  L  G  T   S  M  K   A  L  I

CAAATGCTAG AGATCTGCAT TGGATTTGTA GTACCCTTTC TTATTATGGG         650
Q  M  L  E   I  C  I   G  F  V   V  P  F  L   I  M  G

GGTGTGCTAC TTTATCACAG CAAGGACACT CATGAAGATG CCAAACATTA         700
 V  C  Y   F  I  T  A   R  T  L   M  K  M   P  N  I  K

AAATATCTCG ACCCCTAAAA GTTCTGCTCA CAGTCGTTAT AGTTTTCATT         750
  I  S  R   P  L  K   V  L  L  T   V  V  I   V  F  I

GTCACTCAAC TGCCTTATAA CATTGTCAAG TTCTGCCGAG CCATAGACAT         800
V  T  Q  L   P  Y  N   I  V  K   F  C  R  A   I  D  I

CATCTACTCC CTGATCACCA GCTGCAACAT GAGCAAACGC ATGGACATCG         850
 I  Y  S   L  I  T  S   C  N  M   S  K  R   M  D  I  A

CCATCCAAGT CACAGAAAGC ATCGCACTCT TTCACAGCTG CCTCAACCCA         900
  I  Q  V   T  E  S   I  A  L  F   H  S  C   L  N  P

ATCCTTTATG TTTTTATGGG AGCATCTTTC AAAAACTACG TTATGAAAGT         950
I  L  Y  V   F  M  G   A  S  F   K  N  Y  V   M  K  V

GGCCAAGAAA TATGGGTCCT GGAGAAGACA GAGACAAAGT GTGGAGGAGT        1000
 A  K  K   Y  G  S  W   R  R  Q   R  Q  S   V  E  E  F

TTCCTTTTGA TTCTGAGGGT CCTACAGAGC CAACCAGTAC TTTTAGCATT        1050
  P  F  D   S  E  G   P  T  E  P   T  S  T   F  S  I

TAAAGGTAAA ACTGCTCTGC CTTTTGCTTG GATACATATG AATGATGCTT        1100
- R  - N   C  S  A   F  C  L   D  T  Y  E   - C  F

TCCCCTCAAA TAAAACATCT GCCTTATTCT GAAAAAAAAA AAAAAAM           1147
 P  L  K   - N  I  C   L  I  L   K  K  K   K  K
```

FIG. 1

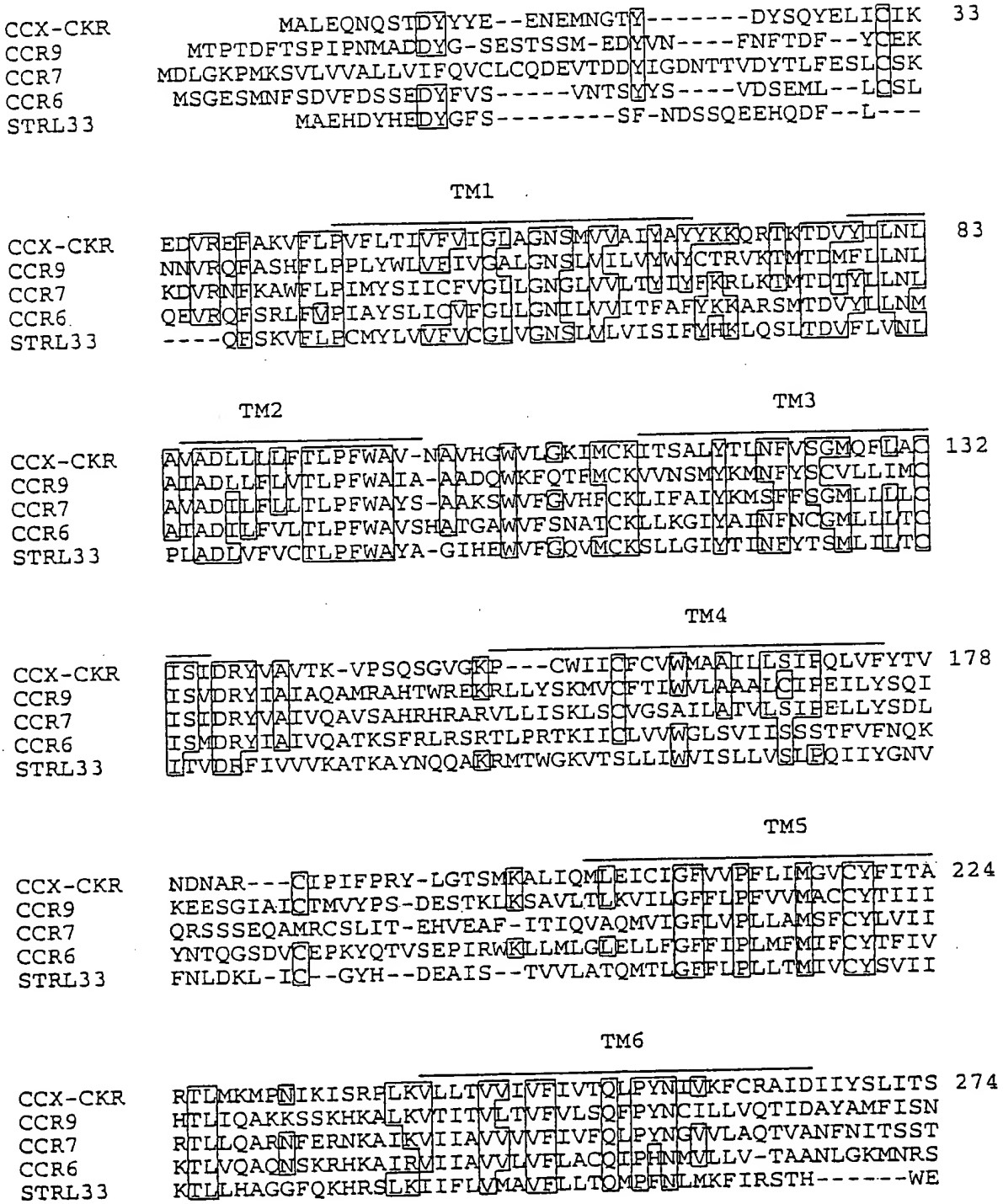


FIG. 2A

```
                                TM7
         CNMSKRMDIAIQVTESIALFHSCLNPILYVFMGASFKNYVMK-------V 317
CCX-CKR  CAVSTNIDICFQVTQTIAFFHSCLNPVLYVFVGERFRRDLVKTLKNLGCI
CCR9     CELSKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCL
CCR7     CQSEKLIGYTKTVTEVLAFLHCCLNPVLYAFIGQKFRNYFLKILKDLWCV
CCR6     YYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFWKLVKDIGCL
STRL33

                                                           350
CCX-CKR  AKKY--GSWRRQRQSVEEFPFDSEGP--TEPTSTFSI
CCR9     SQA-QWVSFTR----REGSLK-LSSMLLETTSGALSL
CCR7     SQE-QLRQWSS----CRHIRR-SSMSVEAETITTFSP
CCR6     RRKYKSSGFSCAGRYSENISRQTSETADNDNASSFTM
STRL33   P--Y--LGVSHQWKSSEDNSKTFSASHNVEATSMFQL
```

FIG. 2A
(CONTINUED)

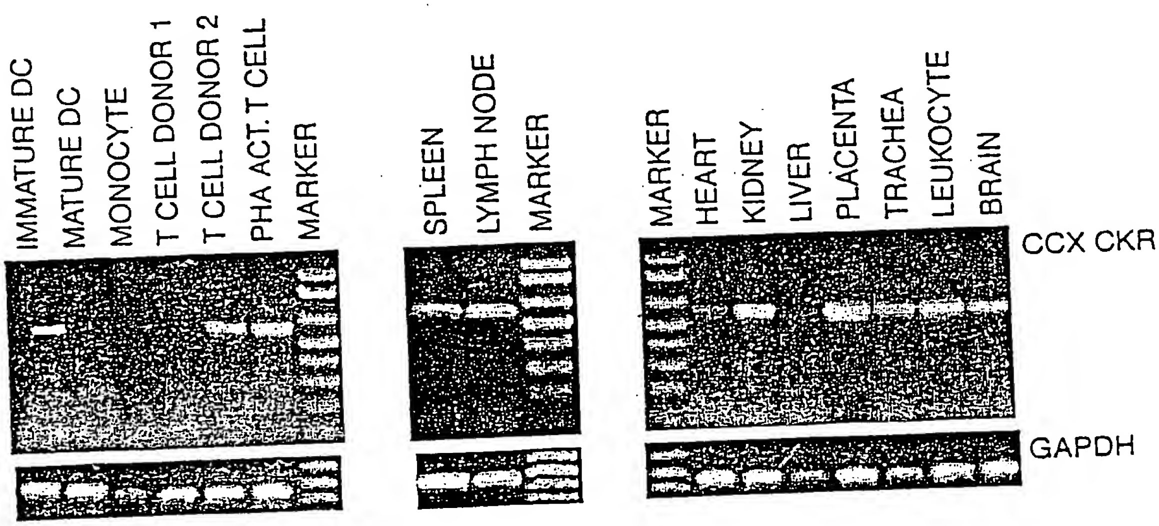


FIG. 2B

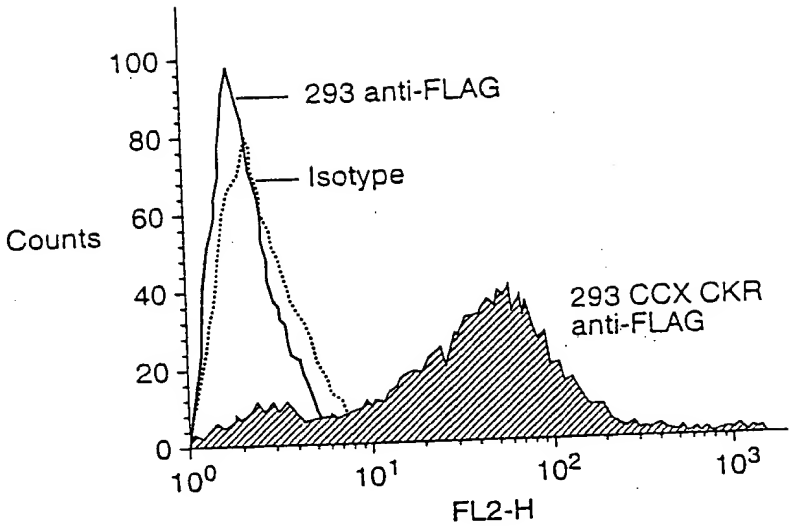


FIG. 2C

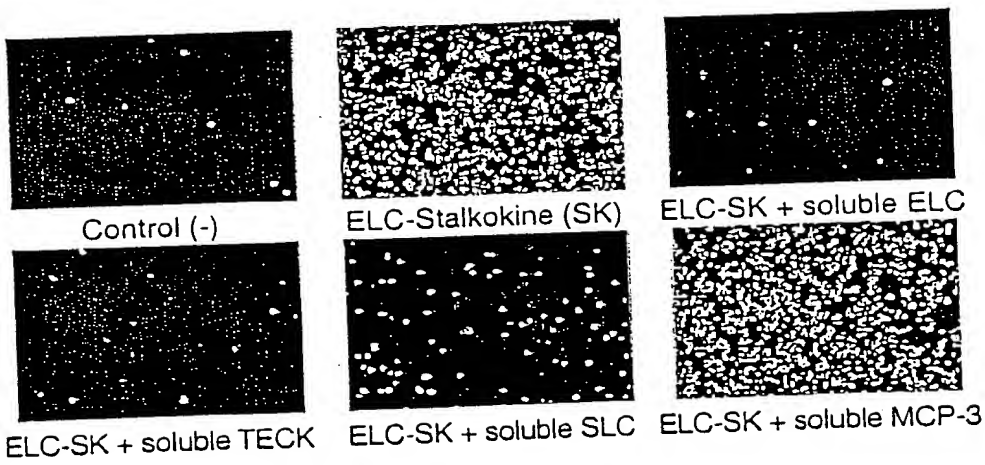


FIG. 3A

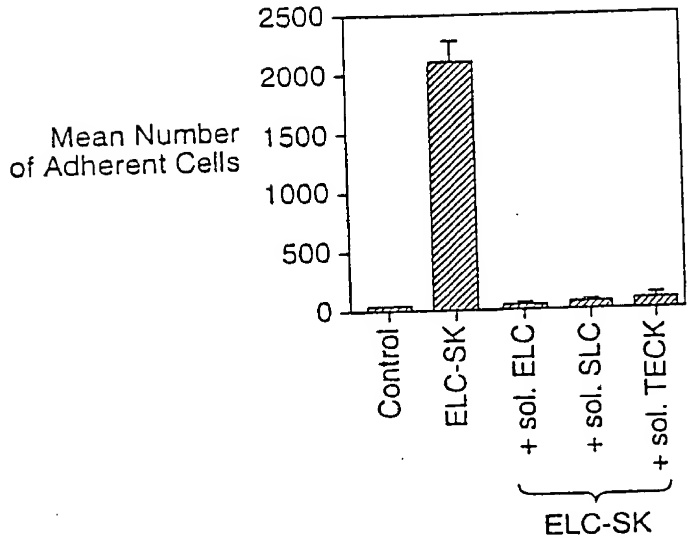


FIG. 3B

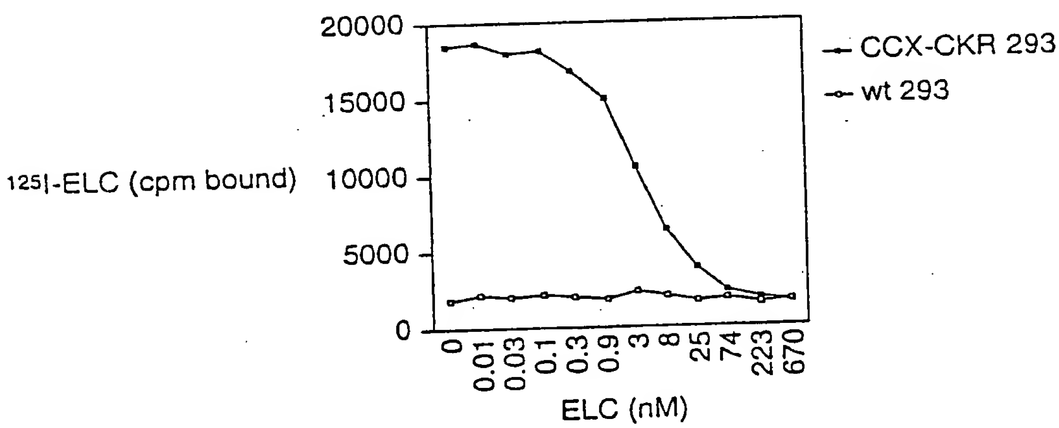


FIG. 3C

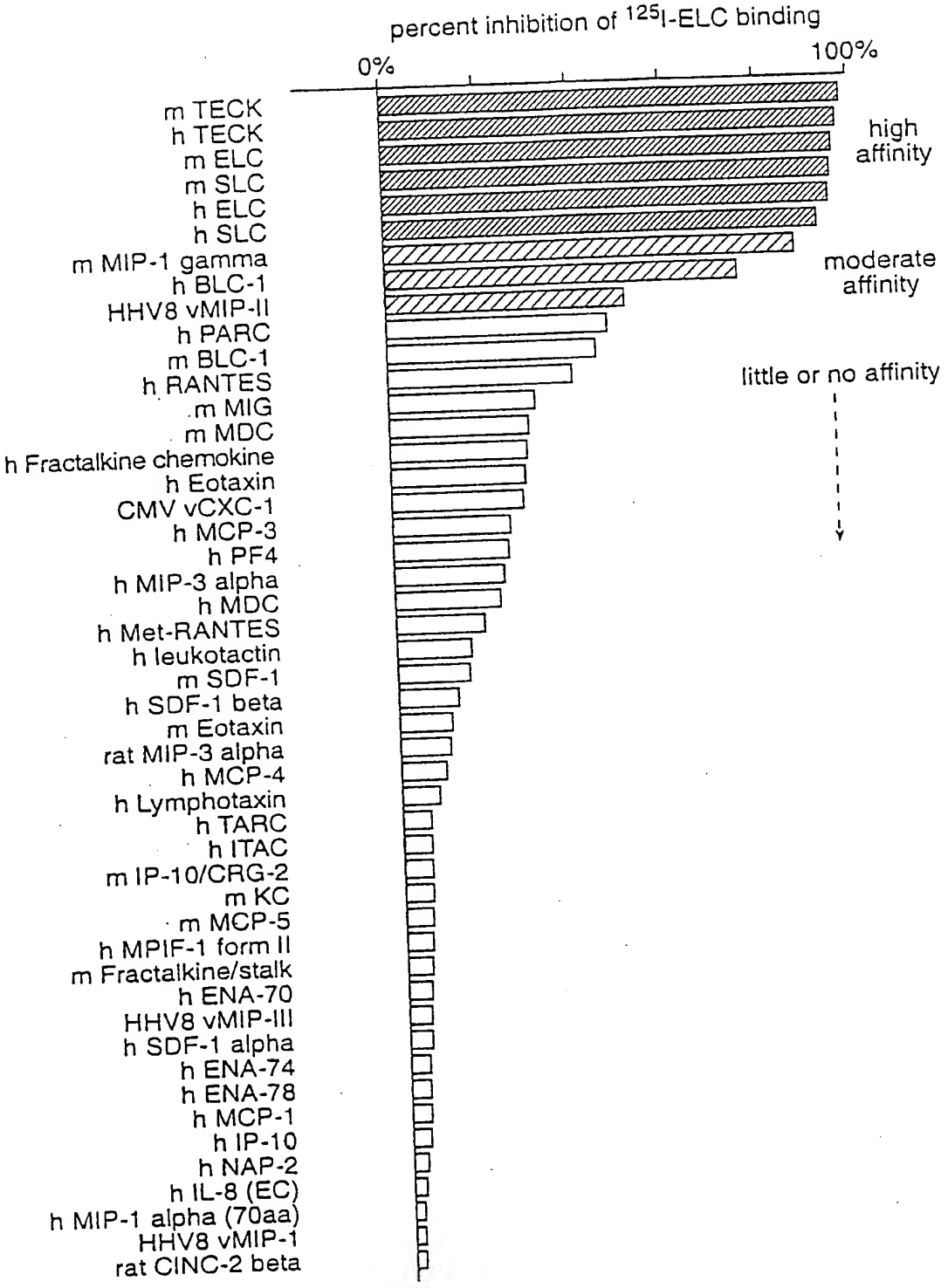


FIG. 4A

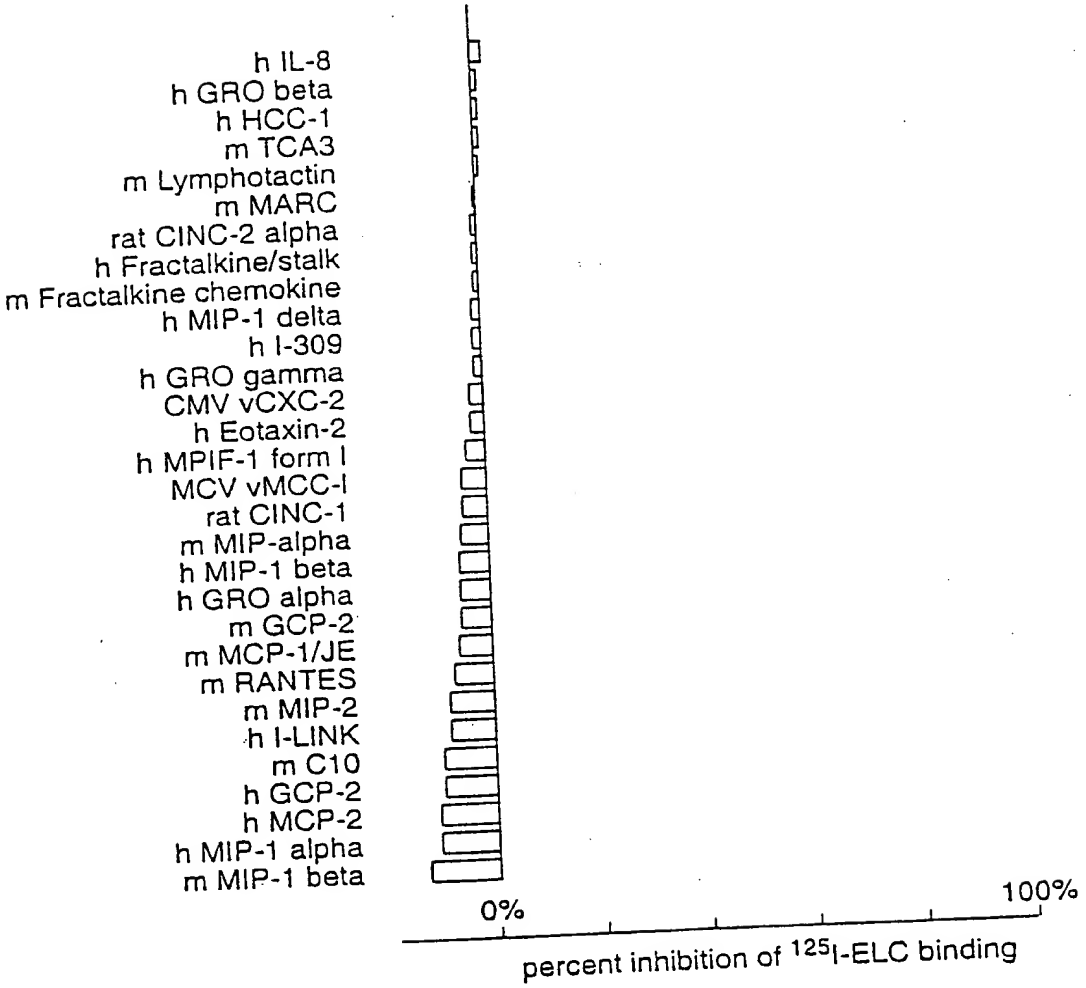
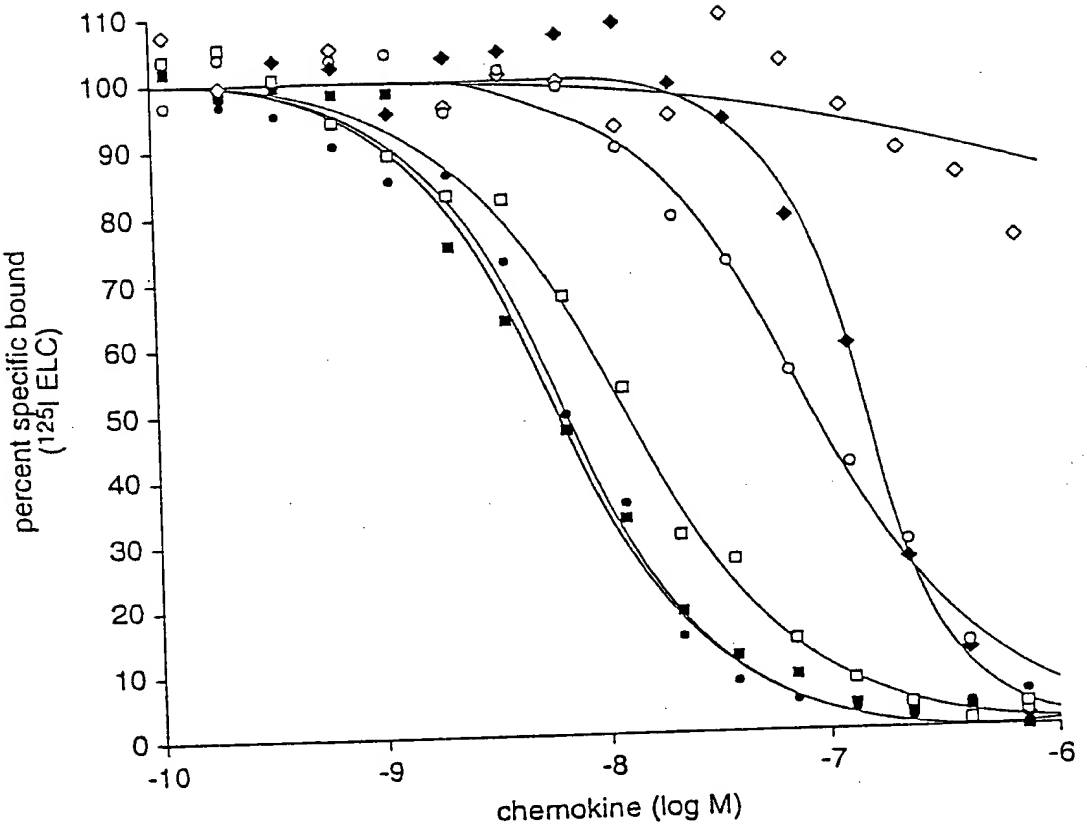


FIG. 4A
(CONTINUED)



human chemokines	IC-50	murine chemokines	IC-50
■ h ELC	6 nM	m ELC	1 nM
□ h SLC	12 nM	m SLC	4 nM
• h TECK	7 nM	m TECK	2 nM
◆ h BLC-1	140 nM	m MIP-1γ	70 nM
○ HHV8 vMIP-II	90 nM		
◇ h MCP-3	>2000 nM		

FIG. 4B

```
5'upstream  ATGCAGCATC TCGTTTATAA AAGGCAACTA GTGAAATTTA GTGCAAATGC  50
CCXCKR      ---------- ---------- ---------- ---------- ----------

5'upstream  TGAGAGAATT TATTTAACTT ATTTAAATTA AATTTATAAA TAACATCAAA 100
CCXCKR      ---------- ---------- ---------- ---------- ----------

5'upstream  ATAAAAAATA AATTTAATTT AAATAAACCA AGTAATTTGC TATTTTCGTT 150
CCXCKR      ---------- ---------- ---------- ---------- ----------

5'upstream  TTTATTCAAT TTGTTGTAGA TATACTTTTA CGATTCACAA AATTATGTAT 200
CCXCKR      ---------- ---------- ---------- ---------- ----------

5'upstream  GTAAAGATTA TAACACTATT TATTCTTTTT AGTTAAAATC TAATTAAATT 250
CCXCKR      ---------- ---------- ---------- ---------- ----------

5'upstream  TTCATATTTT AAAAATCATT TTTACATAAA AGTCTTCACT TTTATTTAGG 300
CCXCKR      ---------- ---------- ---------- ---------- ----------

5'upstream  ATTTAATGAT TAAGAAAATT CTCCAGGGCA TTATGTTTAT TGTCCTGTTC 350
CCXCKR      ---------- ---------- ---------- ---------- ----------

5'upstream  AAATCCAAGC TCTTTCACAC AGAATTGTAC AAGCAAAGTT TGAGTAACTA 400
CCXCKR      ---------- ---------- ---------- ---------- ----------

5'upstream  ATCTTGGGGT CATATTCCAA TGTGGCTCCC ATTAAAGCAT TTCAAAGAGT 450
CCXCKR      ---------- ---------- ---------- ---------- ----------

5'upstream  GCTAGATTCA GGCTCACATA TGTTACAGCA ACAGGCTATA CTCTAGGGAA 500
CCXCKR      ---------- ---------- ---------- ---------- ----------

5'upstream  AGAACAAAAC AGCTTGATAG AAACTGTGTG CTTTTAAGCA TATTTAGACA 550
CCXCKR      ---------- ---------- ---------- ---------- ----------
                                  TRANSLATION START→
5'upstream  AATATCTATC CTGTATTCTC TTTGCCATCT AGATTGGAGC CATGGCTTTG 600
CCXCKR      ---------- ---------- ---------- ---------- -ATGGCTTTG   9

5'upstream  GAACAGAACC -GTCAACAGA TTATTATTAT GAGGAGAAGT GAAATGAATG 649
CCXCKR      GAACAGAACC AGTCAACAGA TTATTATTAT GAGGA-AAAT GAAATGAATG  58

5'upstream  GC-CTCATGA CTACAGTCAG TATGAACTGA TCTGT----- --------TC 685.
CCXCKR      GCACTTATGA CTACAGTCAA TATGAACTGA TCTGTATCAA AGAAGATGTC 108

5'upstream  AGAGAAGAGA CAGAGGATAT GC-ACAGGGT TGCTCCCTGT ATTGCTCACC 734
CCXCKR      AGAGAA---- -------TTT GCAAAAGTTT TCCTCCCTGT ATTCCTCACA 147

5'upstream  ATAG------ ---------- ---------- -------AG- ---------- 740
CCXCKR      ATAGTTTTCG TCATTGGACT TGCAGGCAAT TCCATGGTAG TGGCAATTTA 197

5'upstream  ---------- ---------- ---------- ---------- ---------- 740
CCXCKR      TGCCTATTAC AAGAAACAGA GAACCAAAAC AGATGTGTAC ATCCTGAATT 247

5'upstream  ---------- ---------- ---------- ---------- ---------- 740
CCXCKR      TGGCTGTAGC AGATTTACTC CTTCTATTCA CTCTGCCTTT TTGGGCTGTT 297

5'upstream  ---------- ---------- ---------- ---------- ---------- 740
CCXCKR      AATGCAGTTC ATGGGTGGGT TTTAGGGAAA ATAATGTGCA AAATAACTTC 347
```

FIG. 5

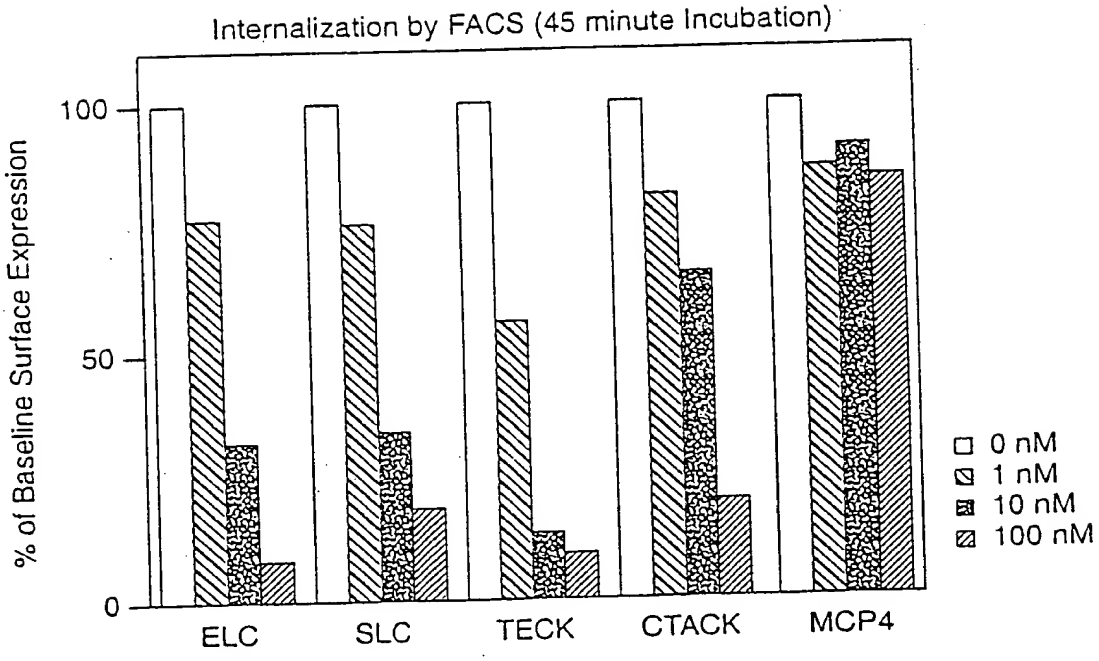


FIG. 6A

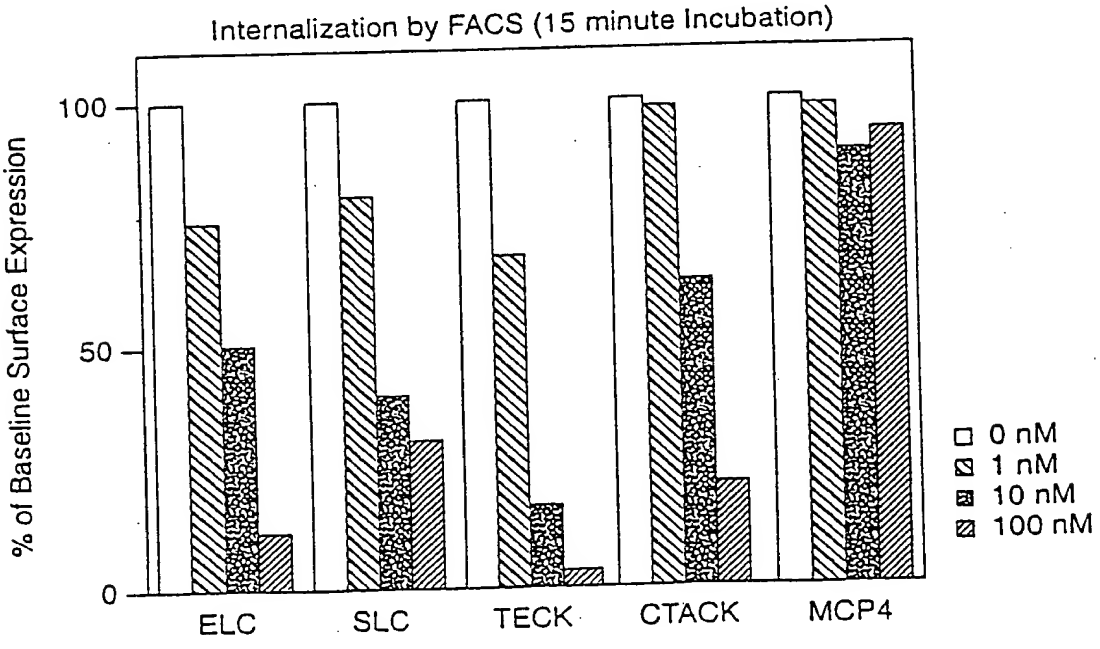


FIG. 6B